

AMENDMENTS TO THE SPECIFICATION

Please amend paragraph [0040] as follows:

A red color ($\lambda_{\text{max}} = 527 \text{ nm}$) was observed in the presence of LiCl (Figure 1A,b and B,b); NaCl (Figure 1A,c and B,c) or RbCl (Figure 1A,e and B,e) and ss-DNA (sequence X1: 5'-GGTTGGTGTGGTTGG-3' (SEQ ID NO 1)). This red color shift is associated with a stoichiometric complexation between the unfolded anionic ss-DNA and the cationic polythiophene derivative (Figure 2, path A). Such stoichiometric polyelectrolyte complexes tend to be insoluble in the medium in which they are formed and appear as aggregates.¹⁵ These red-violet aggregates (probably formed from planar polymer chains) possess an absorption spectrum similar to that obtained in the solid state.

Please amend paragraph [0042] as follows:

In a particular embodiment of the present invention, human α -thrombin was selected as an example of a target to be detected since X1 ss-DNA sequence (5'-GGTTGGTGTGGTTGG-3' (SEQ ID NO 1)) is known to be a specific binding sequence (*i.e.* an aptamer) of this protein. On the other hand, the oligonucleotide ss-DNA (X2: 5'-GGTGGTGGTTGTGGT-3' (SEQ ID NO 2)) is known to be a non-binding sequence.²² A conformational change occurs in the aptamer X1 when it binds to the thrombin molecule. Both NMR and X-ray diffraction studies have revealed that the aptamer adopts a compact unimolecular quadruplex structure with two G-quartets.^{23, 24}

Please amend paragraph [0044] as follows:

The specificity of the detection was verified by two control experiments carried out under identical conditions. In a first control experiment a non-binding sequence ss-DNA (X2: 5'-GGTGGTGGTTGTGGT-3' (SEQ ID NO 2)) was used (Figure 4c) and in a second control experiment BSA (bovine serum albumin) was used (Figure 4d). In both cases, an important red-shift toward lower energy ($\lambda_{\text{max}} = 505 \text{ nm}$) was observed. Furthermore, the color of these solutions was red-violet, which is typical of the planar and highly conjugated structure of the polythiophene backbone when mixed with unfolded ss-DNA (Figure 3, Path B and Figure 2, Path A). The detection limit of this colorimetric method is about 1×10^{-11} mole of thrombin in a total volume of *ca.* 100 μL (a concentration of about $1 \times 10^{-7} \text{ M}$).

Please amend paragraph [0049] as follows:

More specifically, the enantiomeric resolution of D-adenosine and L-adenosine was performed using DNA aptamer (5'-ATTATACCTGGGGGAGTATTGCGGAGGAAGGTATAAT-3' (SEQ ID NO 3)) (31).

Please amend paragraph [0050] as follows:

In a first step, a framework composed of two stacked G-quartets is assumed by mixing D-adenosine and DNA aptamer (31) (5'-ATTATACCTGGGGGAGTATTGCGGAGGAAGGTATAAT-3' (SEQ ID NO 3)). The formed complex is more stable at 5°C. The cationic polymer 1 is then added and is assumed to wrap itself around the previously formed complex. The stoichiometry of the adenosine enantiomer/aptamer/polymer 1 complex is 1:1 1.

Please amend paragraph [0051] as follows:

A series of identical steps was then performed using L-adenosine. Since L-adenosine is not supposed to induce a conformational change in DNA aptamer (31) (5'-ATTATACCTGGGGGAGTATTGCGGAGGAAGGTATAAT-3' (SEQ ID NO 3)), the cationic polymer 1 should bind to the aptamer and lead to the formation of a duplex.

Please enter the Sequence Listing submitted herewith into the specification.